

Please replace the paragraph beginning on page 5, line 24 with the following amended paragraph:

B2

--Figure 2B is a representation of the alternative splicing events (SEQ ID NOS:7, 8, 9, 10, 11, 12, 13, 14, 15 and 16) that result in different C-termini.--

Please replace the paragraph beginning on page 18, line 8 with the following amended paragraph:

--Detailed description of the drawings

Figure 1 shows the genomic sequence of SEQ ID NO:5, wherein exons and introns are designated in the genomic sequence of the present human patched 2 gene. However, exons 12a and 12b discussed above are not specifically shown in Figure 1, but is instead disclosed as the separate sequences SEQ ID NO:3 and SEQ ID NO:4, respectively. Figure 2A discloses an amino acid sequence comparison of the human PTCH2(residues 1-633 of SEQ ID NO:1) (upper lines) and PTCH1(residues 1-699 of SEQ ID NO:6) (lower lines) sequences. Vertical lines indicate identical amino acids, while dots similar amino acids. The PTCH2 sequence presented is composed of the original cDNA clones and of the products of the 5' RACE analysis.--

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B3

Please replace the paragraph beginning on page 18, line 19, with the following amended paragraph:

B4

--Figure 2B is a representation of the alternative splicing events (SEQ ID NOS:7, 8, 9, 10, 11, 12, 13, 14, 15 and 16) that result in different C-termini. In the parotid gland and the colon, the penultimate and the last exon are canonically joined together. In fetal brain however the penultimate exon with part of the 3' intron functions as the terminal exon. The intronic sequence is shown by small letters with the flanking exonic by capital letters. Above the nucleotide sequence, the deduced amino acid sequence is shown, and below is the corresponding sequence of the mouse Ptch2. The conserved intronic dinucleotides are shown by bold letters and the termination signals are indicated by asterisks. Note the absence of conservation of the position of the termination codons between the mouse and human PTCH2 sequences. The putative polyadenylation signals are also shown in this diagram. The genomic organization was obtained by analyzing BAC clones encompassing the PTCH2 gene.--

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Please replace the Sequence Listing filed April 6, 2001 located immediately after the claims with Substitute Sequence Listing enclosed herewith.

#### REMARKS

Enclosed herewith in full compliance to 37 C.F.R. §§1.821-1.825 is a substitute Sequence Listing to be inserted into the specification as indicated above. The substitute Sequence Listing in no way introduces new matter into the specification.